



## SEQUENCE LISTING

<110> Huang, Lan-Qing  
Van Pel, Aline  
Brasseur, Francis  
De Plaen, Etienne  
Boon, Thierry

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att gat gtg aag gaa gtg gac cct gcc ggc cac tcc tac atc ctt gtc Ile Asp Val Lys Glu Val Asp Pro Ala Gly His Ser Tyr Ile Leu Val 170 175 180			2741
acc tgc ctg ggc ctc tcc tat gat ggc ctg ctg ggt gat gat cag agt Thr Cys Leu Gly Leu Ser Tyr Asp Gly Leu Leu Gly Asp Asp Gln Ser 185 190 195			2789
acg ccc aag acc ggc ctc ctg ata atc gtc ctg ggc atg atc tta atg Thr Pro Lys Thr Gly Leu Leu Ile Ile Val Leu Gly Met Ile Leu Met 200 205 210			2837
gag ggc agc cgc gcc ccg gag gag gca atc tgg gaa gca ttg agt gtg Glu Gly Ser Arg Ala Pro Glu Glu Ala Ile Trp Glu Ala Leu Ser Val 215 220 225 230			2885
atg ggg gct gta tga tgggaggag cacagtgtct attggaagct caggaagctg Met Gly Ala Val 235			2940
ctcacccaag agtgggtgca ggagaactac ctggagtacc gccaggcgcc cggcagtgtat cctgtgcgt acgagttctt gtggggtcca agggcccttg ctgaaaccag ctatgtaaaa gtcctggagc atgtggtcag ggtcaatgca agagttcgca tttccctaccc atccctgcata gaagaggctt tggagagaga gaaaggagtt tgagcaggag ttgcagctag ggccagtggg gcaggttgtg ggagggcctg ggccagtgcg cgttccaggg ccacatccac cactttccct gctctgttac atgaggccca ttcttcaactc tgggtttgaa gagagcagtc acagttctca gtatgtggga gcatgttggg tggagggaa cacagtgtgg accatctctc agttcctgtt ctattggcg atttggaggt ttatctttgt ttccctttgg aattgttcca atgttccttc taatggatgg tggatgttcaacattc attttatgtt tgacagttaga cagacttact gcttttata tagtttaga gtaagagtct tgctttcat ttatactggg aaacccatgt tatttcttga attcagacac tacaagagca gaggattaag gtttttttag aatgtaaaa caacatagca gtaaaaataca tgagataaaag acataaaagaa attaaaacaat agttaattct tgccttacct gtacctcta gtgtacccttac tttgttggc ttctttgaga 3720 atgaaattga attaaaatatg aataaataag tccccctgtc cactggctca ttttttccca aaatattcat tgagcttccg ctattggaa ggccctgggt tagtattgga gatgctaca 3839			3000 3060 3120 3180 3240 3300 3360 3420 3480 3540 3600 3660 3720 3780 3839

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<220>  
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agaggccctt ctggcatcag aacagcagga acccccacagt tcctggccctt accagccctt 180  
ttgtcagttcc tggagccttg gcctttgcca ggaggctgca ccctgagatg ccctctcaat 240  
ttctccttca gggtcgaga gaacaggcca gocaggaggtt caggaggccc cagagaagca 300

ctgaagaaga cctgtaagta gaccttggtt agggcatcca gggtagtgc cccagctgag	360		
gcctctcaca cgcttcctct ctccccaggc ctgtgggtct caattgccca gctccggccc	420		
acactctcct gctgccctga cctgagtcat c atg ctt ctt ggg cag aag agt	472		
Met Leu Leu Gly Gln Lys Ser			
1	5		
cag cgc tac aag gct gag gaa ggc ctt cag gcc caa gga gag gca cca	520		
Gln Arg Tyr Lys Ala Glu Glu Gly Leu Gln Ala Gln Gly Glu Ala Pro			
10	15	20	
ggg ctt atg gat gtg cag att ccc aca gct gag gag cag aag gct gca	568		
Gly Leu Met Asp Val Gln Ile Pro Thr Ala Glu Glu Gln Lys Ala Ala			
25	30	35	
tcc tcc tcc tct act ctg atc atg gga acc ctt gag gag gtg act gat	616		
Ser Ser Ser Thr Leu Ile Met Gly Thr Leu Glu Glu Val Thr Asp			
40	45	50	55
tct ggg tca cca agt cct ccc cag agt cct gag ggt gcc tcc tct tcc	664		
Ser Gly Ser Pro Ser Pro Pro Gln Ser Pro Glu Gly Ala Ser Ser Ser			
60	65	70	
ctg act gtc acc gac agc act ctg tgg agc caa tcc gat gag ggt tcc	712		
Leu Thr Val Thr Asp Ser Thr Leu Trp Ser Gln Ser Asp Glu Gly Ser			
75	80	85	
agc agc aat gaa gag gag ggg cca agc acc tcc ccg gac cca gct cac	760		
Ser Ser Asn Glu Glu Gly Pro Ser Thr Ser Pro Asp Pro Ala His			
90	95	100	
ctg gag tcc ctg ttc cgg gaa gca ctt gat gag aaa gtg gct gag tta	808		
Leu Glu Ser Leu Phe Arg Glu Ala Leu Asp Glu Lys Val Ala Glu Leu			
105	110	115	
gtt cgt ttc ctg ctc cgc aaa tat caa att aag gag ccg gtc aca aag	856		
Val Arg Phe Leu Leu Arg Lys Tyr Gln Ile Lys Glu Pro Val Thr Lys			
120	125	130	135
gca gaa atg ctt gag agt gtc atc aaa aat tac aag aac cac ttt cct	904		
Ala Glu Met Leu Glu Ser Val Ile Lys Asn Tyr Lys Asn His Phe Pro			
140	145	150	
gat atc ttc agc aaa gcc tct gag tgc atg cag gtg atc ttt ggc att	952		
Asp Ile Phe Ser Lys Ala Ser Glu Cys Met Gln Val Ile Phe Gly Ile			
155	160	165	
gat gtg aag gaa gtg gac cct gcc ggc cac tcc tac atc ctt gtc acc	1000		
Asp Val Lys Glu Val Asp Pro Ala Gly His Ser Tyr Ile Leu Val Thr			
170	175	180	
tgc ctg ggc ctc tcc tat gat ggc ctg ctg ggt gat gat cag agt acg	1048		
Cys Leu Gly Leu Ser Tyr Asp Gly Leu Leu Gly Asp Asp Gln Ser Thr			
185	190	195	
ccc aag acc ggc ctc ctg ata atc gtc ctg ggc atg atc tta atg gag	1096		
Pro Lys Thr Gly Leu Leu Ile Ile Val Leu Gly Met Ile Leu Met Glu			
200	205	210	215
ggc agc cgc gcc ccg gag gag gca atc tgg gaa gca ttg agt gtg atg	1144		
Gly Ser Arg Ala Pro Glu Glu Ala Ile Trp Glu Ala Leu Ser Val Met			
220	225	230	

ggg gct gta tcatggagg gagcacagtg tctattggaa gctcaggaag 1193  
Gly Ala Val

ctgctcaccc aagagtgggt gcaggagaac tacctggagt accgccaggc gcccggcagt 1253  
gatcctgtgc gctacgagtt cctgtgggt ccaaggccc ttgctgaaac cagctatgtg 1313  
aaagtccctgg agcatgtggt cagggtcaat gcaagagttc gcatttccta cccatccctg 1373  
catgaagagg ctggggaga ggagaaagga gtttgagcag gagttgcagc tagggccagt 1433  
ggggcagggt gtgggagggc ctggggcagt gcacgttcca gggccacatc caccacttc 1493  
cctgctctgt tacatgaggc ccattttca ctctgtgtt gaagagagca gtcacagttc 1553  
tcagtagtgg ggagcatgtt ggggtgtgagg gaacacagtg tggaccatct ctcagttcct 1613  
gttctattgg gcgatttggg ggttatctt tggttcctt tggaaattgtt ccaatgttcc 1673  
ttctaatggg tgggtgtaatg aacttcaaca ttcattttat gtatgacagt agacagactt 1733  
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tgttatttct tgaattc 1810

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ttctcaggggg acagggagag caagaggtca agagctgtgg gacaccacag agcagcactg 180  
aaggagaaga cctgtaagtt ggccttggtt agaacctcca ggggtgtgggtt ctcagctgtg 240  
gccacttaca ccctccctct ctccccaggc ctgtgggtcc ccatcgccca agtcctgccc 300

acactccac ctgctaccct gatcagagtc atc atg cct cga gct cca aag cgt 354  
Met Pro Arg Ala Pro Lys Arg  
1 5

cag cgc tgc atg cct gaa gaa gat ctt caa tcc caa agt gag aca cag 402  
Gln Arg Cys Met Pro Glu Glu Asp Leu Gln Ser Gln Ser Glu Thr Gln  
10 15 20

ggc ctc gag ggt gca cag gct ccc ctg gct gtg gag gag gat gct tca 450  
Gly Leu Glu Gly Ala Gln Ala Pro Leu Ala Val Glu Glu Asp Ala Ser  
25 30 35

tca tcc act tcc acc agc tcc tct ttt cca tcc tct ttt ccc tcc tcc 498  
Ser Ser Thr Ser Thr Ser Ser Phe Pro Ser Ser Phe Pro Ser Ser  
40 45 50 55

tcc tct tcc tcc tcc tcc tgc tat cct cta ata cca agc acc cca 546  
Ser Ser Ser Ser Ser Ser Cys Tyr Pro Leu Ile Pro Ser Thr Pro  
60 65 70

gag gag gtt tct gct gat gat gag aca cca aat cct ccc cag agt gct 594  
Glu Glu Val Ser Ala Asp Asp Glu Thr Pro Asn Pro Pro Gln Ser Ala  
75 80 85

cag ata gcc tgc tcc tcc ccc tcg gtc gtt gct tcc ctt cca tta gat 642  
Gln Ile Ala Cys Ser Ser Pro Ser Val Val Ala Ser Leu Pro Leu Asp  
90 95 100

caa tct gat gag ggc tcc agc agc caa aag gag gag agt cca agc acc	690
Gln Ser Asp Glu Gly Ser Ser Gln Lys Glu Glu Ser Pro Ser Thr	
105 110 115	
cta cag gtc ctg cca gac agt gag tct tta ccc aga agt gag ata gat	738
Leu Gln Val Leu Pro Asp Ser Glu Ser Leu Pro Arg Ser Glu Ile Asp	
120 125 130 135	
gaa aag gtg act gat ttg gtg cag ttt ctg ctc ttc aag tat caa atg	786
Glu Lys Val Thr Asp Leu Val Gln Phe Leu Leu Phe Lys Tyr Gln Met	
140 145 150	
aag gag ccg atc aca aag gca gaa ata ctg gag agt gtc ata aaa aat	834
Lys Glu Pro Ile Thr Lys Ala Glu Ile Leu Glu Ser Val Ile Lys Asn	
155 160 165	
tat gaa gac cac ttc cct ttg ttg ttt agt gaa gcc tcc gag tgc atg	882
Tyr Glu Asp His Phe Pro Leu Leu Phe Ser Glu Ala Ser Glu Cys Met	
170 175 180	
ctg ctg gtc ttt ggc att gat gta aag gaa gtg gat cc	920
Leu Leu Val Phe Gly Ile Asp Val Lys Glu Val Asp	
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<400> 14  
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<210> 15  
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<400> 15  
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1 5 10

<210> 16  
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Val Leu Pro Asp Val Phe Ile Arg Cys  
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Val Leu Pro Asp Val Phe Ile Arg Cys Val  
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<210> 18  
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Ser Glu Ile Trp Arg Asp Ile Asp Phe  
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Tyr Glu Ile Trp Arg Asp Ile Asp Phe  
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<210> 42  
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<400> 42  
Gly Leu Tyr Asp Gly Met Glu His Leu  
1 5

<210> 43  
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<400> 43  
Gly Leu Tyr Asp Gly Arg Glu His Ser  
1 5

<210> 44  
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<400> 44  
Gly Leu Tyr Asp Gly Met Glu His Leu Ile  
1 5 10

<210> 45  
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Gly Leu Tyr Asp Gly Arg Glu His Ser Val  
1 5 10

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1 5

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1 5 10

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Phe Leu Leu Phe Lys Tyr Gln Met Lys  
1 5

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29

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31

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gctctagagc ttagcactcg gaggcttcac t

31

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<210> 55  
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<212> DNA  
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21

<210> 56  
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23

<210> 57  
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<400> 57

Cys Leu Gly Leu Ser Tyr Asp Gly Leu  
1               5